

A genome-wide association study of young horse test traits in Swedish Warmblood

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Aim of study

To find genomic regions associated with conformation and performance traits in Swedish Warmblood (SWB)

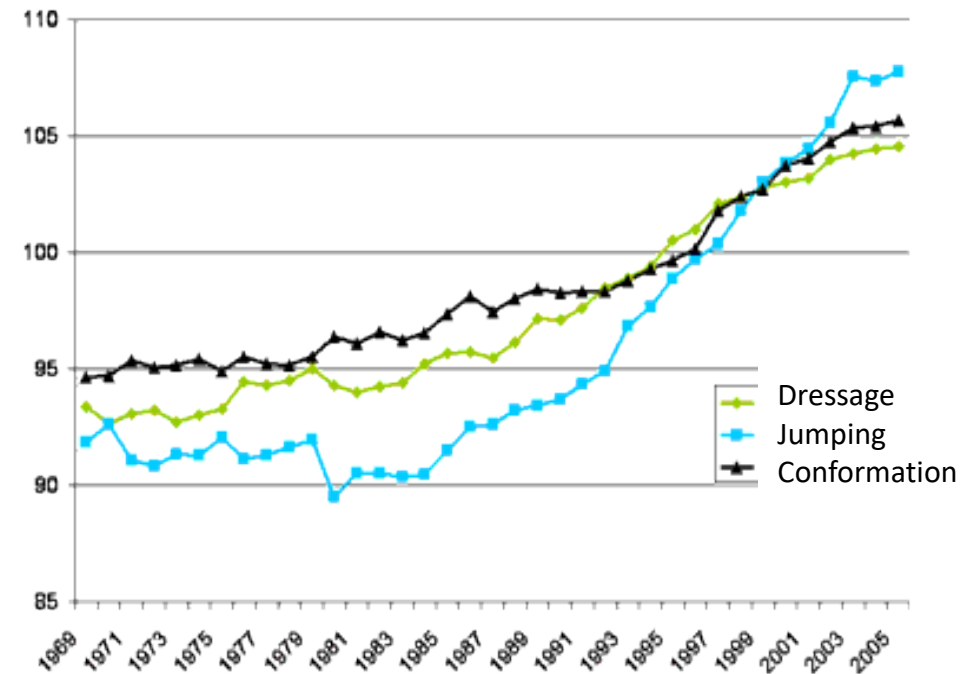
-“A ...horse, which by its good temperament, rideability, good movements and/or jumping ability is internationally competitive”



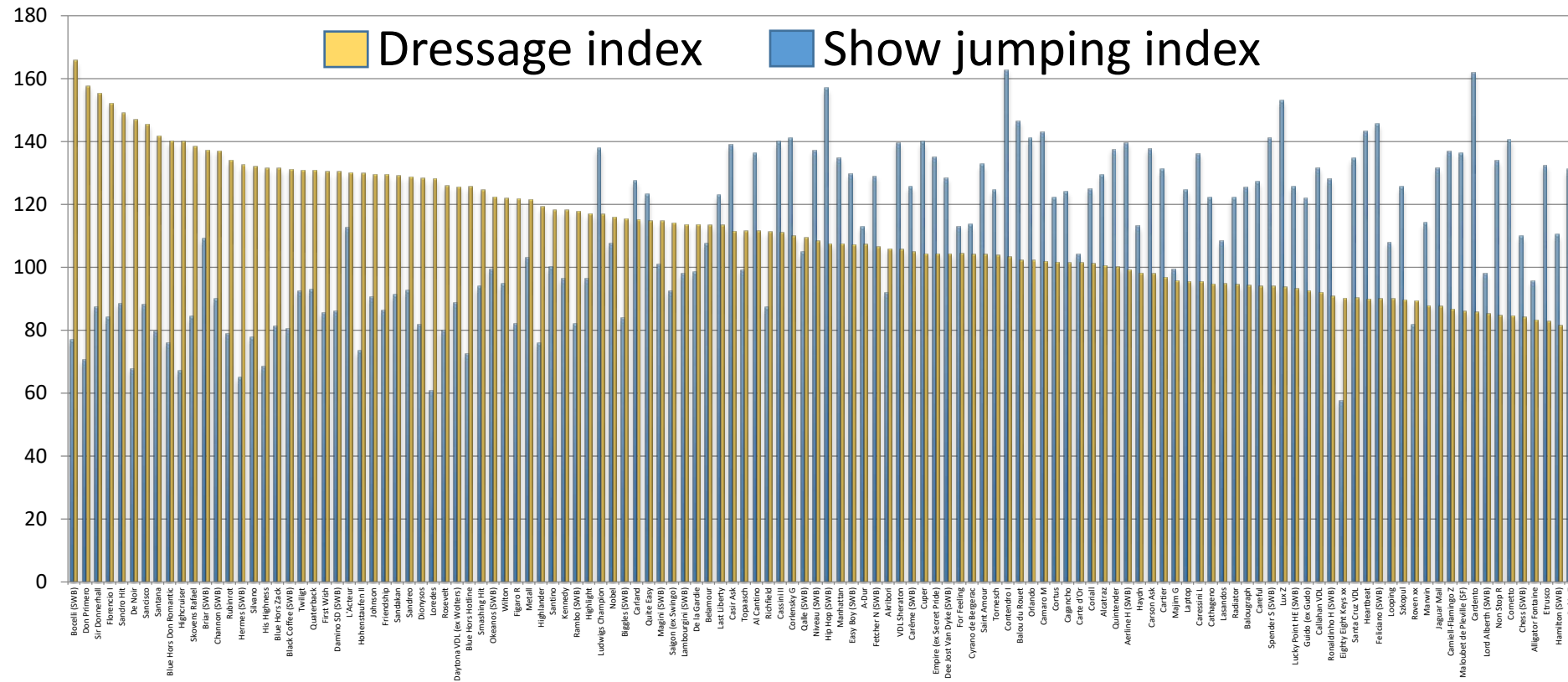
Photo: Maria Håkansson.

Background

- SWB selected for show jumping **and** dressage traits.
- Weak positive genetic correlations previously estimated between jumping and dressage traits.
- Breeders focus increasingly on one discipline rather than both.
- Still, some stallions have high EBVs for both disciplines.



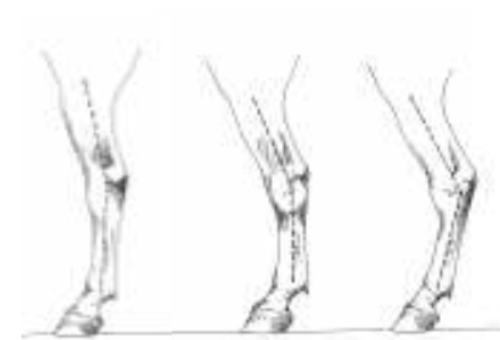
SWB stallions by dressage index



Stallions with ≥ 10 offspring born 2006-2009

Test for 3-year-old SWB

- ~40% of all 3-year-olds are tested for conformation, movements, and jumping.
- Traditional evaluating traits according to breeding goal (scale 1-10), h^2 0.09 - 0.85.
- Linear profiling protocol (scale 1-9) introduced 2013, h^2 0.05 -0.70. Certain deviations marked (0/1).



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39	Take off: direction	upwards	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	forwards	
40	Technique: foreleg	bent	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	hanging	<input type="checkbox"/> under the body <input type="checkbox"/> stretched out

Material & Methods



- 380 horses tested as 3-year-olds 2013-2014, hair-samples.
- Total of 97 young horse test traits
 - Height at withers (cm)
 - 8 traditional evaluating scores
 - 2 summarized traits: show jumping and dressage talent
 - 57 linearly scored traits
 - 29 deviations scored as 0/1
- Genotyped using the equine 670K SNP-chip (Affymetrix).

Material & Methods

- Quality control and analyses in GenABEL, R.
- After QC 379 horses and 467,606 SNPs remained.
- Fast score test for association, with genomic control.
- λ -values generally highest for jumping traits.
- Model included effects of
 - sex (male/female)
 - event (year x location).
- (Analyses taking relationships into account on to-do-list.)



Photo: Carin Wrange

Two main clusters

Cluster 1:

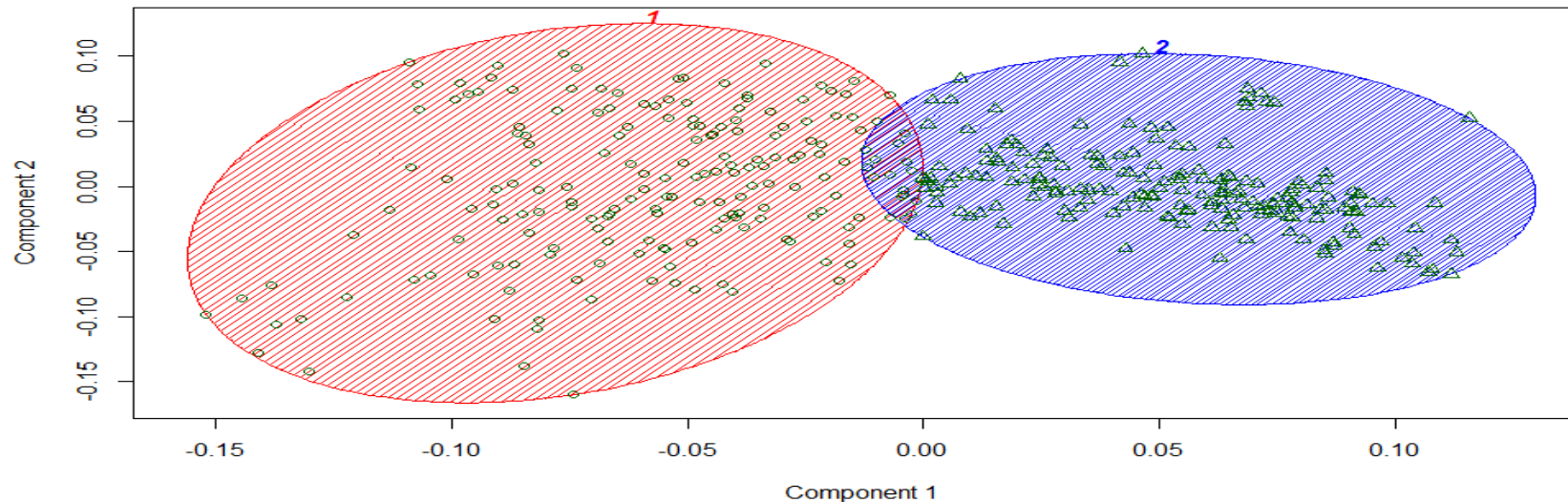
\bar{x} EBV (**dressage**) = 117

\bar{x} EBV (show jumping) = 84

Cluster 2:

\bar{x} EBV (dressage) = 97

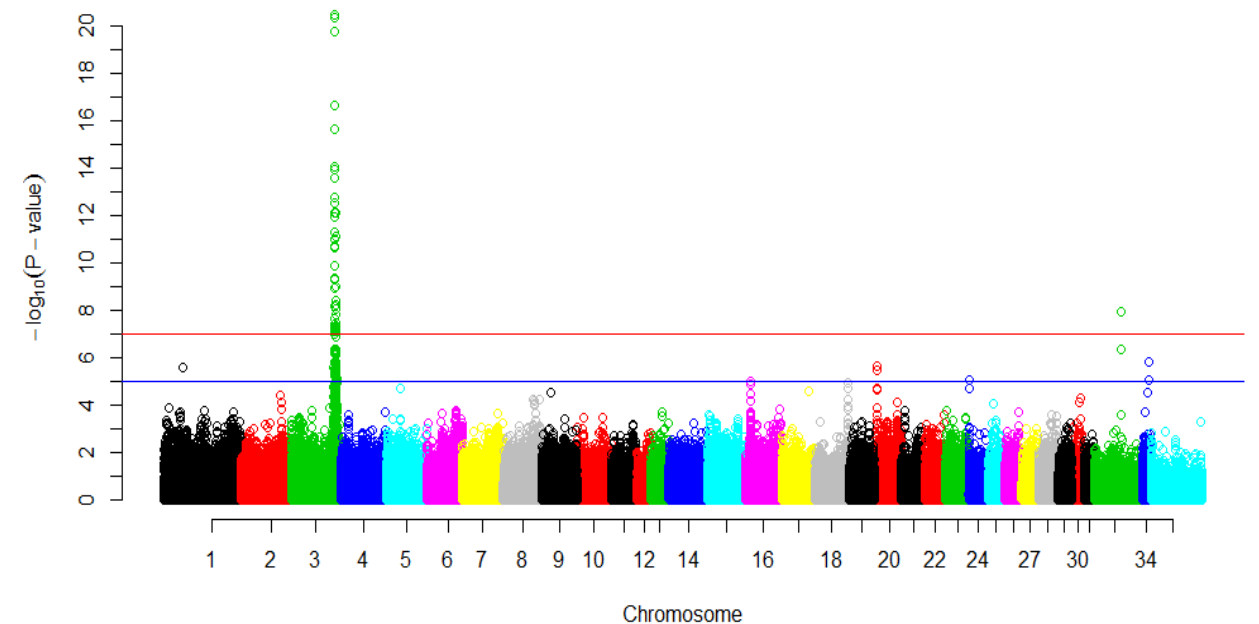
\bar{x} EBV (**show jumping**) = 123



Genotyped horses, born 2010-2011

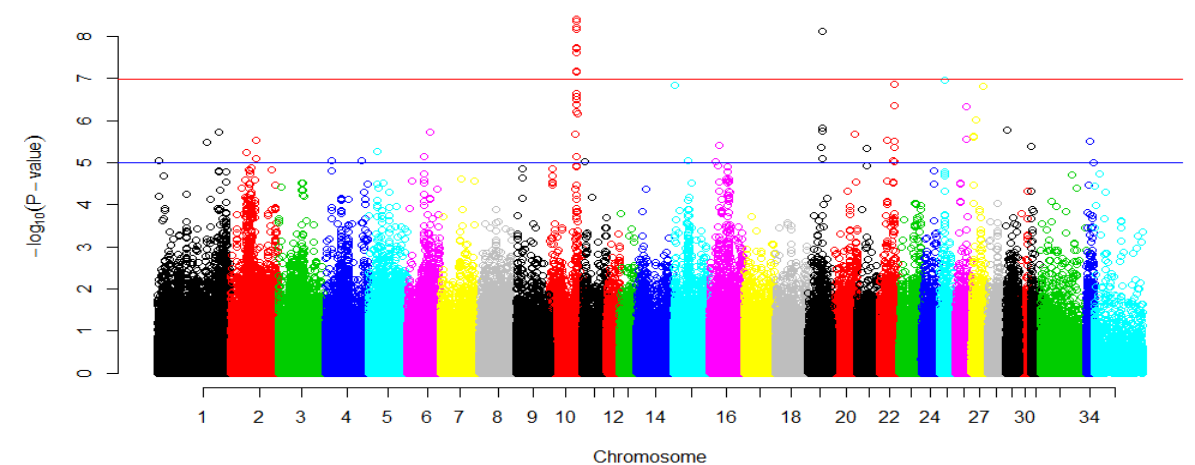
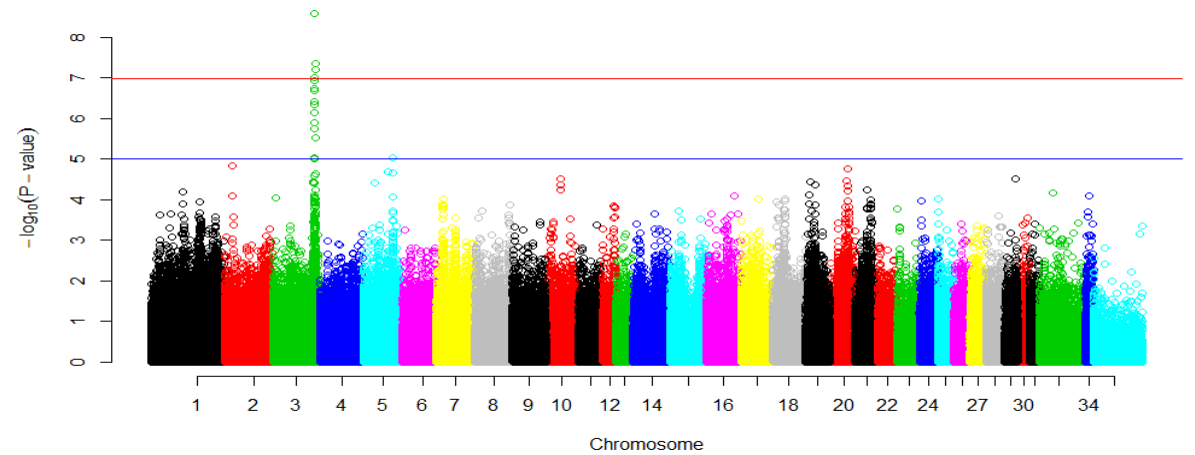
Results - Height at withers

- Confirmed published region on ECA3 highly significant for height at withers ($p=3.4 \times 10^{-21}$).
- LCORL/NCAPG associated with growth and height in horses and other species.
- Proof of concept.



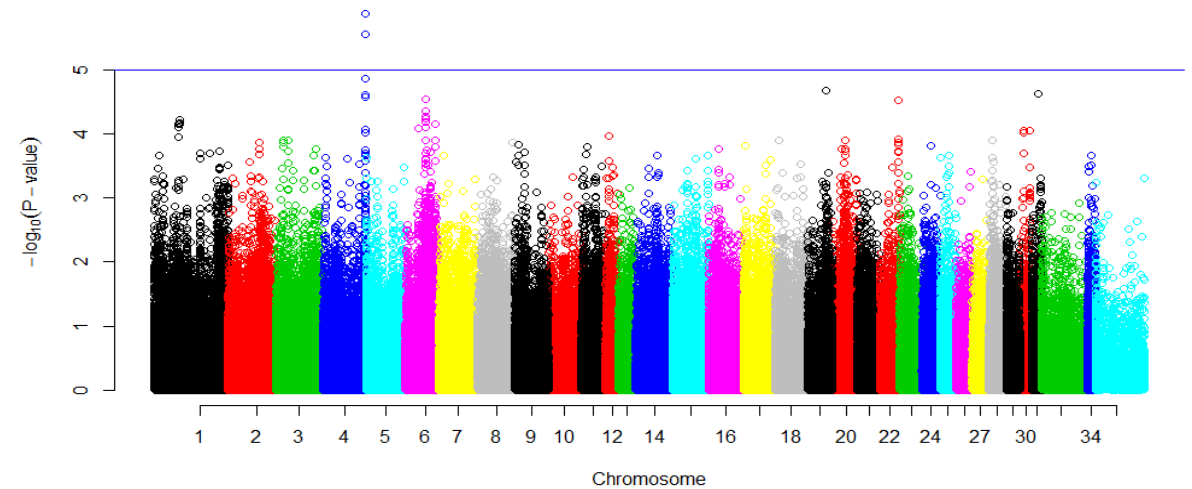
Conformation trait examples

- Significant peak in linear conformation trait ($p = 2.6 \times 10^{-9}$) on ECA3.
- Potentially interesting regions for deviation traits (0/1). Generally few individuals in one of the categories.



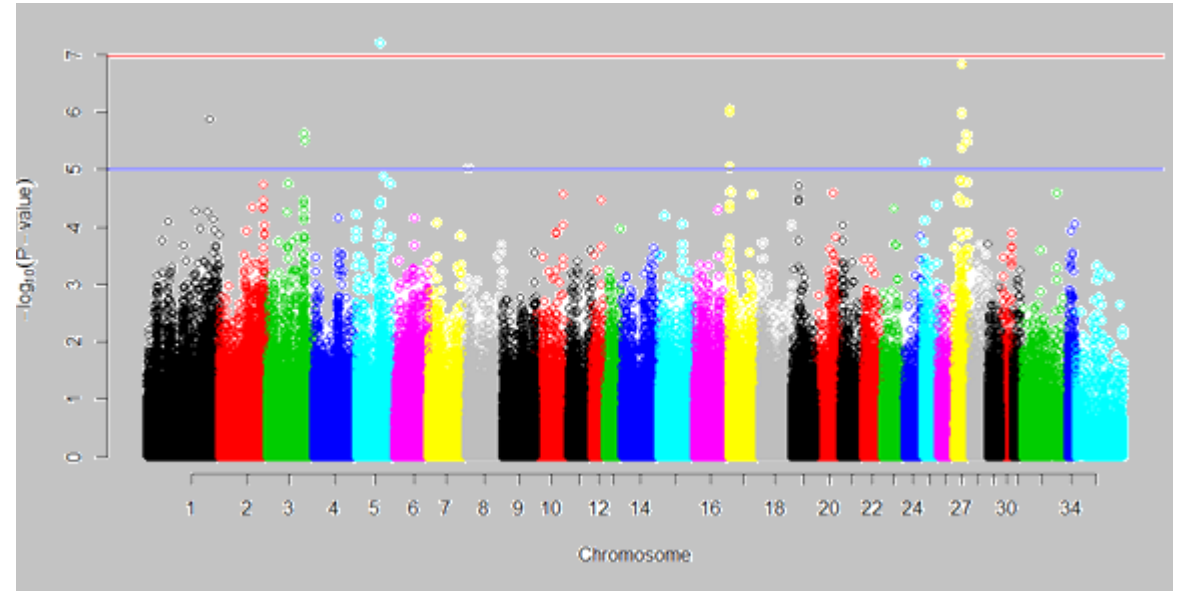
Movement trait example

- Only few suggestive associations for movement traits in spite of high heritabilities ($p=1.3 \times 10^{-6}$)



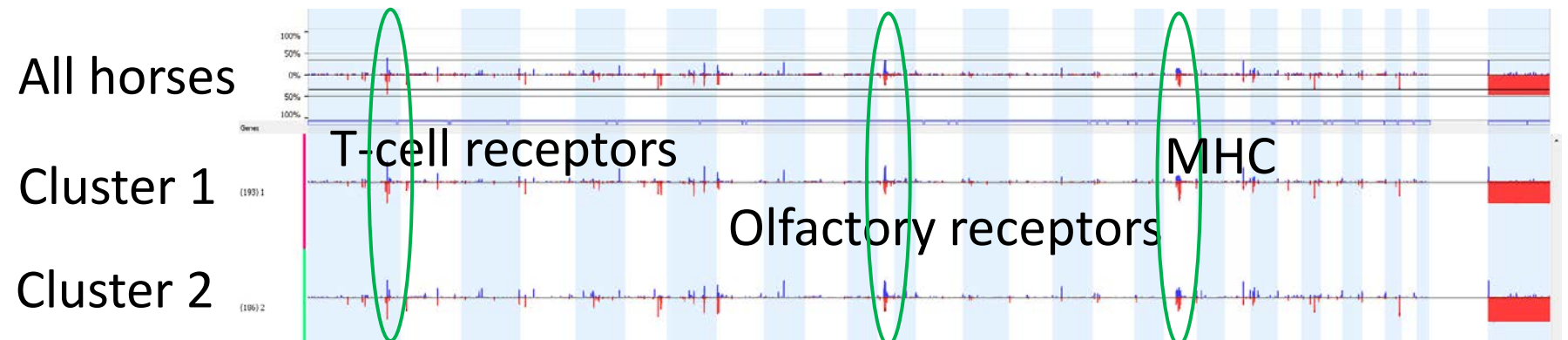
Show Jumping trait example

- No significant association found in full data set (N=378) or in cluster 1.
- But potentially interesting association(s) in cluster 2 only for linear jumping trait (N=189, $p = 6.4 \times 10^{-8}$)



Copy Number Variations in SWB

- Affymetrix raw data files from 670k-SNP genotyping.
- Prel. analysis using BioDiscovery's SNP-FASST2 Segmentation Algorithm. Significance testing for aberrant copy number.
- Gene families known for high CNVs are clearly visible, other chromosomal regions are under investigation.



Conclusions

- Increasing focus towards *either* show jumping *or* dressage among SWB-breeders.
- With 380 horses and 670K SNP-chip genome-wide assoc. for ‘normally distributed’ traits could be detected.
- A highly significant genome-wide association was found for height at ECA3.
- SNP-associations significant after Bonferroni correction was found for conformation traits.
- Within one of two clusters, significant association was found for a linear jumping trait.



Photo: Carin Wrangle

Thank you for listening!



Photo: Julio Gonzalez, SLU

And thanks for contributions from:

- Hanna Göransson-Kultimaa & Anders Isaksson at SciLifeLab
- Swedish Warmblood Association 
- Swedish-Norwegian Foundation for Equine Research 